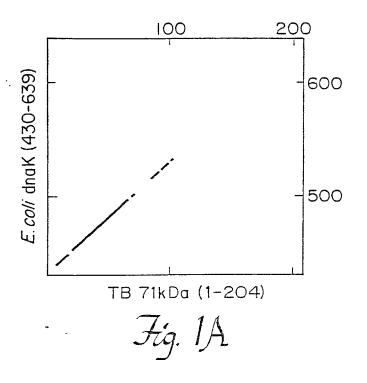
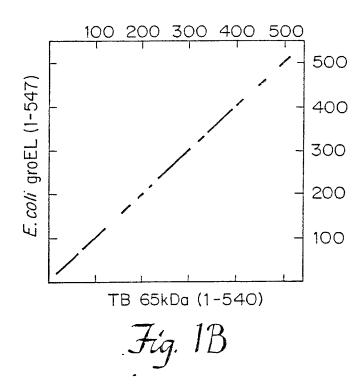


App No.: 10/046,649

Title: Stress Proteins and Uses Therefor

Inventors: Richard A. Young, et al.







MLRLPTVFRQMRPVSRVLAPHLTRAYAKDVKFGADARALMLQGVDLLADAVAVTMGPKGRTVIIEQSWGS

HUMP1

09

50

Title: Stress Proteins and Uses Therefor Inventors: Richard A. Young, *et al.*

-AKDVKFGNDARVKMLRGVNVLADAVKVTLGPKGRNVVLDKSFGA PKVTKDGVTVAKSIDLKDKYKNIGAKLVQDVANNTNEEAGDGTTTATVLARSIAKEGFEKISKGANPVEI PTITKDGVSVAREIEPEDKFENMGAQMVKEVASKANDAAGDGTTTATVLAQAIITEGLKAVAAGMNPMDL RRGVMLAVDAVIAELKKQSKPVTTPEEIAQVATISANGDKEIGNIISDAMKKVGRKGVITVKDGKTLNDE KRGIDKAVTAAVEELKALSVPCSDSKAIAQVGTISANSDETVGKLIAEAMDKVGKEGVITVEDGTGLQDE LEIIEGMKFDRGYISPYFINTSKGQKCEFQDAYVLLSEKKISSIQSIVPALEIANAHRKPLVIIAEDVDG 350 LDVVEGMQFDRGYLSPYFINKPETGAVELESPFILLADKKISNIREMLPVL**EAVAKAGKP**LLIIAEDVEG TKDDAMLLKGKGDKAQIEKRIQEIIEQLDVTTSEYEKEKLNERLAKLSDGVAVLKVGGTSDVEVNEKKDR NKDTTTI I DGVGEEAA I QGRVAQ I RQQ I EEATSDYDREKLQERVAKLAGGVAV I KVGAATEVEMKEKKAR EALSTLVLNRLKVGLQVVAVKAPGFGDNRKNQLKDMAIATGGAVFGEEGLTLNLEDVQPHDLGKVGEVIV EALATAVVNTIRGIVKVAAVKAPGFGDRRKAMLQDIATLTGGTVISEE-IGMELEKATLEDLGQAKRVVI 120 190 330 110 180 250 390 100 240 380 90 160 150 GROEL GROEL HUMP1 GROEL GROEL HUMP1 HUMP1 GROEL GROEL HUMP1



App No.: 10/046,649 INFORMATION Title: Stress Proteins and Uses Therefor

Inventors: Richard A. Young, et al.

	421	430	440	450	460	470	480	490
HUMP1	VTDALN	ATRAAVEI	ATRAAVEEGIVLGGGCALLRO	VTDALNATRAAVEEGIVLGGGCALLRCIPALDSLTPANEDQKIGIEIIKRTLKIPAMTIAKNAGVEGSLI	PANEDQKIG	IEIIKRTLE :	KIPAMTIAKNAGV	EGSLI
GROEL	VEDALH	ATRAAVE	EGVVAGGG	VEDALHATRAAVEEGVVAGGGVALIRVASKLADLRGQNEDQNVVSSSL-RAMEAPLRQIVLNCGEEPSVV	GONEDQNVV	SSSL-RAME	SAPLRQIVLNCGE	TPSVV
	491	500	510	520	530	540	550	560
HUMP1	VEKIMÇ	SSSEVGY	DAMAGDFV.	VEKIMQSSSEVGYDANAGDFVNMVEKGIIDPTKVVRTALLDAAGVASLLTTAEVVVTEIPKEEKDPGMGA	RTALLDAAG: ::	VASLLTTAE	SVVVTEIPKEEKD: ::	::
GROEL	ANTVKC	GDGNYGY	NAATEEYG	ANTVKGGDGNYGYNAATEEYGNMIDMGILDPTKVTRSALQYAASVAGLMITTECMVTDLPKND-AADLGA	RSALQYAAS	VAGLMITTE	∃CMVTDLPKND-A	ADLGA
	561	570						
HUMP1	МВВМВС	MGGMGGGMGGGMF	MF					
GROEL	AGGMGG	AGGMGGMGGMM-	₺					
Total score 276 ident	1:t1:	4667, 5 les out o	, 5 breaks it of 545 po	4667, 5 breaks es out of 545 possible matches between		residues		
25 random Aliqnment	25 random runs Aliqnment score	п	65.34 SD	Standard deviation	ation =	18.94	Mean = 3429.48	48



	~ ~	10	20	30	40	20	09	70
HUMP1 ML65K	MLRLP:	TVFRQMRP	/SRVLAPHLTR	MLRLPTVFRQMRPVSRVLAPHLTRAYAKDVKFGADARALMLQGVDLLADAVAVTMGPKGRTV : ::::: : ::::: : MAKTIAYDEEARRGLERGLNSLADAVKVTLGPKGRNV	DARALMLQG :: EARRGLERG	VDLLADAVA::::: LNSLADAVK	YAKDVKFGADARALMLQGVDLLADAVAVTMGPKGRTVIIEQSWGS :: ::::::::::::::::::::::::::::::::::	IIEQSWGS : :: VLEKKWGA
	71	80	06	100	110	120	130	140
HUMP1 ML65K	PKVTK : : PTITN	CDGVTVAKS:	IDLKDKYKNIG : : : :: IELEDPYEKIG	AKLVQDVANN: : :: ::	TNEEAGDGT:::::	TTATVLARS:::::::	PKVTKDGVTVAKSIDLKDKYKNIGAKLVQDVANNTNEEAGDGTTTATVLARSIAKEGFEKISKGANPVEI : ::: :: :: :: :: :: :: :: :: :: ::: :	GANPVEI :::: GANPLGL
	141	150	160	170	180	190	. 200	210
HUMP1 ML65K	RRGVE::	TLAVDAVIAI ::: KAVDKVTE	SLKKQSKPVTT : : : : PLLKDAKEVET	PEEIAQVATI: : :: :: KEQIAATAAI	SANGDKEIG	NIISDAMKK::::::DLIAEAMDK	RRGVMLAVDAVIAELKKQSKPVTTPEEIAQVATISANGDKEIGNIISDAMKKVGRKGVITVKDGKTLNDE :: ::: ::: ::: :::: : KRGIEKAVDKVTETLLKDAKEVETKEQIAATAAISA-GDQSIGDLIAEAMDKVGNEGVITVEESNTFGLQ	GKTLNDE : SNTFGLQ
	211	220	230	240	250	260	270	280
HUMP1 ML65K	LEIIE :: : LELTE	GMKFDRGY];;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;;	ISPYFINTSKG :: :: ISGYFVTDAER	QKCEFQDAYVI : QEAVLEEPYII	LLSEKKISS:::	IQSIVPALE ::: VKDLLPLLE	LEIIEGMKFDRGYISPYFINTSKGQKCEFQDAYVLLSEKKISSIQSIVPALEIANAHRKPLVIIAEDVDG :: ::: :: :: :: :: :: :: :: :: :: :: ::	IAEDVDG::::::
	281	290	300	310	320	330	340	350
HUMP1 NL65K	EALSTI::::EALSTI		EALSTLVLNRLKVGLQVVAVKAPGF ::::::: :::::::::::::::::::::::::::::	FGDNRKNQLKI ::: :: : FGDRRKAMLQI	OMAIATGGA ::::: OMAILTGAQ	VFGEEGLTU: : :: VISEE-VGL	VLNRLKVGLQVVAVKAPGFGDNRKNQLKDMAIATGGAVFGEEGLTLNLEDVQPHDLGKVGEVIV : : ::::::::::::::::::::::::::::::::	KVGEVIV : KARKVVM
	351	360	370	380	390	400	410	420
HUMP1 ML.65K	TKDDA ::: TKDET	MLLKGKGDF : :: TIVEGAGDT	(AQIEKRIQEI : : :	IEQLDVTTSE: :	YEKEKLNER: ::::	LAKLSDGVAVLK:::::::::::::::::::::::::::::::::::	TKDDAMLLKGKGDKAQIEKRIQEIIEQLDVTTSEYEKEKLNERLAKLSDGVAVLKVGGTSDVEVNEKKDR ::: ::::: ::: :: :: :: :: :::::::::::	VNEKKDR : : : LKERKHR
:		: 			ť			



HUMP1	421 , VTDAL	430 ALNATRA	30 4 VAAVEEGIVL	440 , LGGGCALLI	430 440 450 460 470 480 490 490 490 490 490 490 490 490 490 49	460 , PANEDQKI(470 , SIEIIKRTI	4. KIPAMT:	480 , TIAKNAGV	490 . ,
	IED	: AVRNAK	::::::::::::::::::::::::::::::::::::::	GGGVTLL(::::::::::::::::::::::::::::::::::::::	LTGDEAT-(: : : : .: GANIVKVALEAPLR	EAPLKQ	:::: IAFNSGM	: SPGVV
	491	500		510	520	530	540	Ω 3.	550	260
HUMPI		IMQSSS	EVGYDAMAGI	DFVNMVE	VEKIMQSSSEVGYDAMAGDFVNMVEKGIIDPTKVVRTALLDAAGVASLLTTAEVVVTEIPKEEKDPGMGA	RTALLDAAO	SVASLLTTA	EVVVTE)	PKEEKD)	GMGA
	AEK	VRNLSV	GHGLNAATG	EYEDLLKA	AEKVRNLSVGHGLNAATGEYEDLLKAGVADPVKVTRSALQNAASIAGLFTT-EAVVADKPEKTAAPASDP	: :: :: RSALQNAAS	: :: SIAGLFTT-	: :: EAVVADI	: KPEKTAA)	ASDF
	561	570	0,							
	MGG	MGGMGGGMGGGMF	GGMF							
	TGGI	:::::: TGGMGG-MDF	• FI							
tal 255	score = 'identitie	= 4552 ties o	4552, 7 breaks es out of 540 p	s possibl	4552, 7 breaks es out of 540 possible matches between residues	between	residues			
	25 random runs Alignment scor	ns ore =	47.73 SD) Stan	Standard deviation	tion =	23.86		Mean = 3413.16	v



	н ч	H	0	20	30	40	50	09	7.0
HUMP1 TB65K	MLRLP.	PTVFR	QMRPVSR 	VLAPHLTRA!	TVFRQMRPVSRVLAPHLTRAYAKDVKFGADARALMLQGVDLLADAVAVTMGPKGRTVIIEQSWGS : :::::::::::::::::::::::::::::::::::	RALMLQGVDLI : RRGLERGLNAI	LADAVAVTMG	GPKGRTVIIEQS:::::::::::::::::::::::::::::::::::	WGS :: WGA
	71	90	0 `	06	100	110	120	130	140
нимр1 тв65к	PKVTKI : : : PTITNI	TKDGVT: ::	VAKSIDL :::: IAKEIEL	KDKYKNIGAI : : ::: EDPYEKIGAI	DGVTVAKSIDLKDKYKNIGAKLVQDVANNTNEEAGDGTTTATVLARSIAKEGFEKISKGANPVEI::::::::::::::::::::::::::::::::::::	EEAGDGTTTATVLA::::::::::::::::::::::::::::::::	FVLARSIAKE	GFEKISKGANP : ::: GLRNVAAGANP	/EI
,	141	150	0 •	160	170	180	190	200	210
нимР1 ТВ65К	RRGVM] :: KRGIE	/MLAVD. :: :EKAVE:	AVIAELK : KVTETLL	KQSKPVTTPI : : : KGAKEVETKI	RRGVMLAVDAVIAELKKQSKPVTTPEEIAQVATISANGDKEIGNIISDAMKKVGRKGVITVKDGKTLNDE :: :: :: :: :: :: : : : : : : : : : :	NGDKEIGNII: :: :: -GDQSIGDLII	SDAMKKVGRK(::::: AEAMDKVGNE	GVITVKDGKTL :::::: GVITVEESNTF	NDE 3LQ
	211	220	0 -	230	240	250	260	270	280
HUMP1 TB65K	LEIIEC :: :: LELTEC	LEIIEGMKFDRGY :: :: :: :: LELTEGMRFDKGY	DRGYISP : ::: DKGYISG	YFINTSKGQ! :: YFVTDPERQE	GMKFDRGYISPYFINTSKGQKCEFQDAYVLLSEKKISSIQSIVPALEIANAHRKPLVIIAEDVDG :: ::::: :: :: :: :: :: :: :: :: :: ::	SEKKISSIQS: : : /SSKVSTVKDI	IVPALEIANAI : :: :LPLLEKVIG	HRKPLVIIAEDVDG ::: ::::::	/DG : : /EG
	281	29(0 ,	300	310	320	330	340	350
HUMP1 PB65K	EALSTI ::::: EALSTI	TLVLNI TLVVNI	RLKVGLQ KIRGTFK,	VVAVKAPGFC ::::::: SVAVKAPGFC	LVLNRLKVGLQVVAVKAPGFGDNRKNQLKDMAIATGGAVFGEEGLTLNLEDVQPHDLGKVGEVIV :: : :::::::::::::::::::::::::::::::	AIATGGAVFGE :: :: : : AILTGGQVISE	SEGLTLNLED'S :: :: :: :: :: :: :: :: :: :: :: :: ::	VQPHDLGKVGE ::: ADLSLLGKARK	71V
	351	360	0.	370	380	390	400	410	420
HUMP1 TB65K	TKDE :::	AMLLKO TTIVE	GKGDKAQ : :: GAGDTDA	IEKRIQEIII : : IAGRVAQIRÇ	TKDDAMLLKGKGDKAQIEKRIQEIIEQLDVTTSEYEKEKLNERLAKLSDGVAVLKVGGTSDVEVNEKKDR::: ::::::::::::::::::::::::::::::::	KEKLNERLAKI ::: :::: REKLQERLAKI	SDGVAVLKV	GGTSDVEVNEK : :: : GAATEVELKER	(DR : : (HR



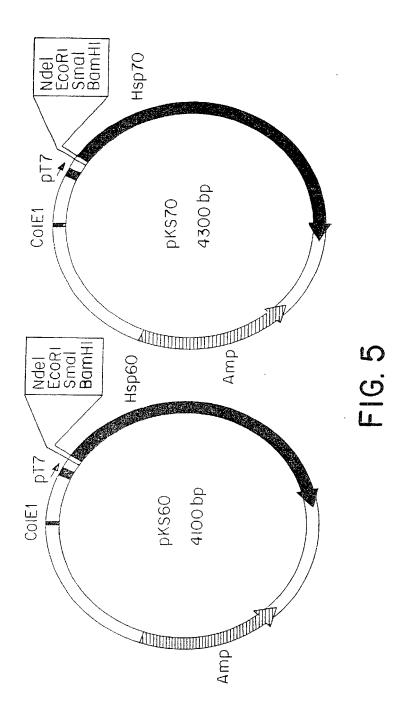
App No.: 10/046,649 10145645 1015 1015 Title: Stress Proteins and Uses Therefor

Inventors:

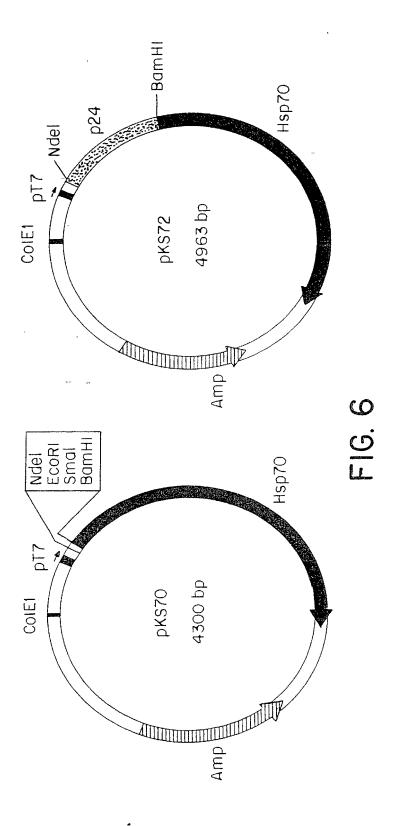
Richard A. Young, et al.

	421	430	440	450	460	470	480	490
HUMP1	VTDALN	ATRAAVEEG	IVLGGGCALLR(CIPALDSLTP	ANEDQKIGI	EIIKRTLE	VTDALNATRAAVEEGIVLGGGCALLRCIPALDSLTPANEDQKIGIEIIKRTLKIPAMTIAKNAGVEGSLI	EGSLI
TB65K	:: IEDAVRI	::::: NAKAAVEEG	AAVEEGIVAGGGVTLLQAAPTLDELK-	: :: : AAPTLDELK-	: : LEGDEATGA	: : : : TGANIVKVALEAPLK	: ::::::::::::::::::::::::::::::::::::	: EPGVV
	491	500	510	520	530	540	550	560
HUMP1	VEKIMO	SSSEVGYDAI	MAGDFVNMVEKO	SIIDPTKVVR	TALLDAAGV	ASLLTTAE	VEKIMQSSSEVGYDAMAGDFVNMVEKGIIDPTKVVRTALLDAAGVASLLTTAEVVVTEIPKEEKDPGMGA	PGMGA
TB65K	AEKVRN	: LPAGHGLNA(: QTGVYEDLLAAC	: :: :: : : : : : : : : : : : : : : :	SALQNAASI	AGLFLTTE	:: :: : : : : : : : : : : : : : : : :	: SVPG-
	561	570						
HUMP1	MGGMGG	MGGMGGGMGGGMF						
TB65K	::	:::::: GGDMGGMDF						
Total 257	score = 4 identities	560, 5 bres s out of !	Total score = 4560, 5 breaks 257 identities out of 540 possible matches between residue	matches	between r	esidues		
25 ran Aliqum	25 random runs Alignment score =	= 49.36 SD	5 SD Stand	Standard deviation =	tion =	23.23	23.23 Mean = 3413.16	91









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